

cgctctagcc cggtggaaag ctttcatcca gaaca atg aat ttc ata aag gac	53
Met Asn Phe Ile Lys Asp	
1 5	
aat agc cga gcc ctt att caa aga atg gga atg act gtt ata aag caa	101
Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys Gln	
10 15 20	
atc aca gat gac cta ttt gta tgg aat gtt ctg aat cgc gaa gaa gta	149
Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val	
25 30 35	
aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg atc	197
Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly Ile	
40 45 50	
att cac atg att ttg aaa aag ggt tca gag tcc tgt aac ctc ttt ctt	245
Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe Leu	
55 60 65 70	
aaa tcc ctt aag gag tgg aac tat cct cta ttt cag gac ttg aat gga	293
Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu Phe Gln Asp Leu Asn Gly	
75 80 85	
caa agt ctt ttt cat cag aca tca gaa gga gac ttg gac gat ttg gct	341
Gln Ser Leu Phe His Gln Thr Ser Glu Gly Asp Leu Asp Asp Leu Ala	
90 95 100	
cag gat tta aag gac ttg tac cat acc cca tct ttt ctg aac ttt tat	389
Gln Asp Leu Lys Asp Leu Tyr His Thr Pro Ser Phe Leu Asn Phe Tyr	
105 110 115	
ccc ctt ggt gaa gat att gac att att ttt aac ttg aaa agc acc ttc	437
Pro Leu Gly Glu Asp Ile Asp Ile Ile Phe Asn Leu Lys Ser Thr Phe	
120 125 130	
aca gaa cct gtc ctg tgg agg aag gac caa cac cat cac cgc gtg gag	485
Thr Glu Pro Val Leu Trp Arg Lys Asp Gln His His Arg Val Glu	
135 140 145 150	
cag ctg acc ctg aat ggc ctc ctg cag gct ctt cag agc ccc tgc atc	533
Gln Leu Thr Leu Asn Gly Leu Leu Gln Ala Leu Gln Ser Pro Cys Ile	
155 160 165	
att gaa ggg gaa tct ggc aaa ggc aag tcc act ctg ctg cag cgc att	581
Ile Glu Gly Glu Ser Gly Lys Ser Thr Leu Leu Gln Arg Ile	
170 175 180	
gcc atg ctc tgg ggc tcc gga aag tgc aag gct ctg acc aag ttc aaa	629
Ala Met Leu Trp Gly Ser Gly Lys Cys Lys Ala Leu Thr Lys Phe Lys	
185 190 195	
ttc gtc ttc ttc ctc cgt ctc agc agg gcc cag ggt gga ctt ttt gaa	677
Phe Val Phe Phe Leu Arg Leu Ser Arg Ala Gln Gly Gly Leu Phe Glu	
200 205 210	

Fig. 1A

acc ctc tgt gat caa ctc ctg gat ata cct ggc aca atc agg aag cag		725
Thr Leu Cys Asp Gln Leu Leu Asp Ile Pro Gly Thr Ile Arg Lys Gln		
215	220	225
230		
aca ttc atg gcc atg ctg ctg aag ctg cgg cag agg gtt ctt ttc ctt		773
Thr Phe Met Ala Met Leu Leu Lys Leu Arg Gln Arg Val Leu Phe Leu		
235	240	245
ctt gat ggc tac aat gaa ttc aag ccc cag aac tgc cca gaa atc gaa		821
Leu Asp Gly Tyr Asn Glu Phe Lys Pro Gln Asn Cys Pro Glu Ile Glu		
250	255	260
gcc ctg ata aag gaa aac cac cgc ttc aag aac atg gtc atc gtc acc		869
Ala Leu Ile Lys Glu Asn His Arg Phe Lys Asn Met Val Ile Val Thr		
265	270	275
act acc act gag tgc ctg agg cac ata cgg cag ttt ggt gcc ctg act		917
Thr Thr Thr Glu Cys Leu Arg His Ile Arg Gln Phe Gly Ala Leu Thr		
280	285	290
gct gag gtg ggg gat atg aca gaa gac agc gcc cag gct ctc atc cga		965
Ala Glu Val Gly Asp Met Thr Glu Asp Ser Ala Gln Ala Leu Ile Arg		
295	300	305
310		
gaa gtg ctg atc aag gag ctt gct gaa ggc ttg ttg ctc caa att cag		1013
Glu Val Leu Ile Lys Glu Leu Ala Glu Gly Leu Leu Leu Gln Ile Gln		
315	320	325
aaa tcc agg tgc ttg agg aat ctc atg aag acc cct ctc ttt gtg gtc		1061
Lys Ser Arg Cys Leu Arg Asn Leu Met Lys Thr Pro Leu Phe Val Val		
330	335	340
atc act tgt gca atc cag atg ggt gaa agt gag ttc cac tct cac aca		1109
Ile Thr Cys Ala Ile Gln Met Gly Glu Ser Glu Phe His Ser His Thr		
345	350	355
caa aca acg ctg ttc cat acc ttc tat gat ctg ttg ata cag aaa aac		1157
Gln Thr Thr Leu Phe His Thr Phe Tyr Asp Leu Leu Ile Gln Lys Asn		
360	365	370
aaa cac aaa cat aaa ggt gtg gct gca agt gac ttc att cgg agc ctg		1205
Lys His Lys His Lys Gly Val Ala Ala Ser Asp Phe Ile Arg Ser Leu		
375	380	385
390		
gac cac tgt gga gac cta gct ctg gag ggt gtg ttc tcc cac aag ttt		1253
Asp His Cys Gly Asp Leu Ala Leu Glu Gly Val Phe Ser His Lys Phe		
395	400	405
gat ttc gaa ctg cag gat gtg tcc agc gtg aat gag gat gtc ctg ctg		1301
Asp Phe Glu Leu Gln Asp Val Ser Ser Val Asn Glu Asp Val Leu Leu		
410	415	420
aca act ggg ctc ctc tgt aaa tat aca gct caa agg ttc aag cca aag		1349
Thr Thr Gly Leu Leu Cys Lys Tyr Thr Ala Gln Arg Phe Lys Pro Lys		
425	430	435

Fig. 1B

DNA sequence analysis

tat aaa ttc ttt cac aag tca ttc cag gag tac aca gca gga cga aga Tyr Lys Phe Phe His Lys Ser Phe Gln Glu Tyr Thr Ala Gly Arg Arg 440 445 450	1397
ctc agc agt tta ttg acg tct cat gag cca gag gag gtg acc aag ggg Leu Ser Ser Leu Leu Thr Ser His Glu Pro Glu Glu Val Thr Lys Gly 455 460 465 470	1445
aat ggt tac ttg cag aaa atg gtt tcc att tcg gac att aca tcc act Asn Gly Tyr Leu Gln Lys Met Val Ser Ile Ser Asp Ile Thr Ser Thr 475 480 485	1493
tat agc agc ctg ctc cgg tac acc tgt ggg tca tct gtg gaa gcc acc Tyr Ser Ser Leu Leu Arg Tyr Thr Cys Gly Ser Ser Val Glu Ala Thr 490 495 500	1541
agg gct gtt atg aag cac ctc gca gca gtg tat caa cac ggc tgc ctt Arg Ala Val Met Lys His Leu Ala Ala Val Tyr Gln His Gly Cys Leu 505 510 515	1589
ctc gga ctt tcc atc gcc aag agg cct ctc tgg aga cag gaa tct ttg Leu Gly Leu Ser Ile Ala Lys Arg Pro Leu Trp Arg Gln Glu Ser Leu 520 525 530	1637
caa agt gtg aaa aac acc act gag caa gaa att ctg aaa gcc ata aac Gln Ser Val Lys Asn Thr Thr Glu Gln Glu Ile Leu Lys Ala Ile Asn 535 540 545 550	1685
atc aat tcc ttt gta gag tgt ggc atc cat tta tat caa gag agt aca Ile Asn Ser Phe Val Glu Cys Gly Ile His Leu Tyr Gln Glu Ser Thr 555 560 565	1733
tcc aaa tca gcc ctg agc caa gaa ttt gaa gct ttc ttt caa ggt aaa Ser Lys Ser Ala Leu Ser Gln Glu Phe Glu Ala Phe Phe Gln Gly Lys 570 575 580	1781
agc tta tat atc aac tca ggg aac atc ccc gat tac tta ttt gac ttc Ser Leu Tyr Ile Asn Ser Gly Asn Ile Pro Asp Tyr Leu Phe Asp Phe 585 590 595	1829
ttt gaa cat ttg ccc aat tgt gca agt gct ctg gac ttc att aaa ctg Phe Glu His Leu Pro Asn Cys Ala Ser Ala Leu Asp Phe Ile Lys Leu 600 605 610	1877
gac ttt tat ggg gga gct atg gct tca tgg gaa aag gct gca gaa gac Asp Phe Tyr Gly Gly Ala Met Ala Ser Trp Glu Lys Ala Ala Glu Asp 615 620 625 630	1925
aca ggt gga atc cac atg gaa gag gcc cca gaa acc tac att ccc agc Thr Gly Gly Ile His Met Glu Glu Ala Pro Glu Thr Tyr Ile Pro Ser 635 640 645	1973
agg gct gta tct ttg ttc aac tgg aag cag gaa ttc agg act ctg Arg Ala Val Ser Leu Phe Phe Asn Trp Lys Gln Glu Phe Arg Thr Leu 650 655 660	2021

Fig. 1C

gag gtc aca ctc cggttc agc aag ttg aat aag caa gat atc aca Glu Val Thr Leu Arg Asp Phe Ser Lys Leu Asn Lys Gln Asp Ile Thr 665 670 675	2069
tat ctg ggg aaa ata ttc agc tct gcc aca agc ctc agg ctg caa ata Tyr Leu Gly Lys Ile Phe Ser Ser Ala Thr Ser Leu Arg Leu Gln Ile 680 685 690	2117
aag aga tgt gct ggt gtg gct gga agc ctc agt ttg gtc ctc agc acc Lys Arg Cys Ala Gly Val Ala Gly Ser Leu Ser Leu Val Leu Ser Thr 695 700 705 710	2165
tgt aag aac att tat tct ctc atg gtg gaa gcc agt ccc ctc acc ata Cys Lys Asn Ile Tyr Ser Leu Met Val Glu Ala Ser Pro Leu Thr Ile 715 720 725	2213
gaa gat gag agg cac atc aca tct gta aca aac ctg aaa acc ttg agt Glu Asp Glu Arg His Ile Thr Ser Val Thr Asn Leu Lys Thr Leu Ser 730 735 740	2261
att cat gac cta cag aat caa cggtcg ccgggtt ctg act gac agc Ile His Asp Leu Gln Asn Gln Arg Leu Pro Gly Gly Leu Thr Asp Ser 745 750 755	2309
ttg ggt aac ttg aag aac ctt aca aag ctc ata atg gat aac ata aag Leu Gly Asn Leu Lys Asn Leu Thr Lys Leu Ile Met Asp Asn Ile Lys 760 765 770	2357
atg aat gaa gaa gat gct ata aaa cta gct gaa ggc ctg aaa aac ctg Met Asn Glu Glu Asp Ala Ile Lys Leu Ala Glu Gly Leu Lys Asn Leu 775 780 785 790	2405
aag aag atg tgt tta ttt cat ttg acc cac ttg tct gac att gga gag Lys Lys Met Cys Leu Phe His Leu Thr His Leu Ser Asp Ile Gly Glu 795 800 805	2453
gga atg gat tac ata gtc aag tct ctg tca agt gaa ccc tgt gac ctt Gly Met Asp Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro Cys Asp Leu 810 815 820	2501
gaa gaa att caa tta gtc tcc tgc ttg tct gca aat gca gtg aaa Glu Glu Ile Gln Leu Val Ser Cys Cys Leu Ser Ala Asn Ala Val Lys 825 830 835	2549
atc cta gct cag aat ctt cac aat ttg gtc aaa ctg agc att ctt gat Ile Leu Ala Gln Asn Leu His Asn Leu Val Lys Leu Ser Ile Leu Asp 840 845 850	2597
tta tca gaa aat tac ctg gaa aaa gat gga aat gaa gct ctt cat gaa Leu Ser Glu Asn Tyr Leu Glu Lys Asp Gly Asn Glu Ala Leu His Glu 855 860 865 870	2645
ctg atc gac agg atg aac gtg cta gaa cag ctc acc gca ctg atg ctg Leu Ile Asp Arg Met Asn Val Leu Glu Gln Leu Thr Ala Leu Met Leu 875 880 885	2693

Fig. 1D

ccc tgg ggc tgt gac gtg caa ggc agc ctg agc agc ctg ttg aaa cat Pro Trp Gly Cys Asp Val Gln Gly Ser Leu Ser Ser Leu Leu Lys His 890 895 900	2741
ttg gag gag gtc cca caa ctc gtc aag ctt ggg ttg aaa aac tgg aga Leu Glu Glu Val Pro Gln Leu Val Lys Leu Gly Leu Lys Asn Trp Arg 905 910 915	2789
ctc aca gat aca gag att aga att tta ggt gca ttt ttt gga aag aac Leu Thr Asp Thr Glu Ile Arg Ile Leu Gly Ala Phe Phe Gly Lys Asn 920 925 930	2837
cct ctg aaa aac ttc cag cag ttg aat ttg gcg gga aat cgt gtg agc Pro Leu Lys Asn Phe Gln Gln Leu Asn Leu Ala Gly Asn Arg Val Ser 935 940 945 950	2885
agt gat gga tgg ctt gcc ttc atg ggt gta ttt gag aat ctt aagcaa Ser Asp Gly Trp Leu Ala Phe Met Gly Val Phe Glu Asn Leu Lys Gln 955 960 965	2933
tta gtg ttt ttt gac ttt agt act aaa gaa ttt cta cct gat cca gca Leu Val Phe Phe Asp Phe Ser Thr Lys Glu Phe Leu Pro Asp Pro Ala 970 975 980	2981
tta gtc aga aaa ctt agc caa gtg tta tcc aag tta act ttt ctg caa Leu Val Arg Lys Leu Ser Gln Val Leu Ser Lys Leu Thr Phe Leu Gln 985 990 995	3029
gaa gct agg ctt gtt ggg tgg caa ttt gat gat gat gat ctc agt gtt Glu Ala Arg Leu Val Gly Trp Gln Phe Asp Asp Asp Asp Leu Ser Val 1000 1005 1010	3077
att aca ggt gct ttt aaa cta gta act gct taa ataaaagtgtatctcgaaaggcca Ile Thr Gly Ala Phe Lys Leu Val Thr Ala *	3130
1015 1020	
gta	3133

Fig. 1E

1 ATGCTGAACGCTGGTCCCCTGGCTCCCTATTTCTCTATACTTTGTCTCTGTGTCTTTCTTT
 TACGACTTGCACCAGGGACCCGAGGAATAAGAAAGAGATATGAAACAGAGACACAGAAAAGAAAA
 10 M L N A G P L G S L I S F S I L C L C V F F F

 71 CCAAGTCTCGTTCACCTAACGAGAACACCCACAGAACAGAAGGTATCTGGTCTACAAGAACTCGA
 GTTCAAGAGCAAGGTGGATTGCTTTGGGTGCTTGTCTTCCATAGACCAGATGTTCTGAGCT
 24 D S K S L V P P N E K H P Q N K K V S G L Q E L E

 141 GGCCTCACTGAAACGAAAGCAAATACAAGAACCTTATTTAAAAACATGTCTGGTCTCCAAAGAAC
 CGGAGTGACTTTGCCTTCGTTATGTTCTTGAAATAAAATTGTACAGAACAGAGGGTTCTTC
 47 D A S L K R K A N T K K L Y F K N M S W S P K K

 211 AGGGCAATTGGATTGCTCAGCCAGAGACCCCTGCAGGCAGACACACAAGCGGCTGGACGTCGAGAGGAAC
 TCCCGTTAACCTAACGAGTCGGCTCTGGAACGTCGCTGTGTTGCTGCCGACCTGCAGCTCCTTG
 71 D R A I G L L S Q R P L Q A D T Q A A G R R E E

 281 ACATCGGCGGAAGAACATACAAGCAGCTGGACGTCAGAGGACGTTGAAGGGAGAATGCTGGCGGAAGAG
 TGTAGCCGCCTTCTTGATGTTGCTCGACCTGCAGGTCTCCTGCAACTTCCCTTACGACCGCCTCTC
 94 D H I G G R T Y K Q L D V Q R T L K G E C W R K S

 351 CACACAACAGACATCGGCACGCCAGCAGGCCATCCACCAGAGGAACGACTCGGAGTTGGCCTGGAGGTG
 GTGTGTTGCTGTAGCCGTGCGGTCTCCGGTAGGTGGTCTCTGCTGAGCCTCAAACCGGACCTCCAC
 117 D T Q Q T S A R Q Q A J H Q R N D S E F G L E V

 421 AATTTCATAAAGGACAATAGCCGAGCCCTTATTCAAAGAATGGGAATGACTGTTATAAGCAAATCACAG
 TTAAAGTATTCTCTGTTATCGGCTCGGAATAAGTTCTTACCCCTACTGACAATATTGTTAGTGTC
 141 D N F I K D N S R A L I Q R M G M T V I K Q I T

 491 ATGACCTATTGTATGGAATGTTCTGAATCGGAAGAAGTAAACATCATTGCTGCGAGAAGGTGGAGCA
 TACTGGATAAACATACCTTACAAGACTTAGCGCTCTTCAATTGAGTAAACGACGCTCTCACCTCGT
 64 D D L F V W N V L N R E E V N I I C C E K V E Q

 561 GGATGCTGCTAGAGGATCATCACATGATTGAAAAAGGGTCAGAGTCCTGTAACCTTTCTTAA
 CCTACGACGATCTCCCTAGTAAGTGTACTAAAACCTTCCCAAGTCTCAGGACATTGGAGAAAGAATT
 187 D A A R G I I H M I L K K G S E S C N L F L K

 631 TCCCTTAAGGAGTGGAACTATCCTCTATTTCAGGACTTGAATGGACAAAGTTTGAGGAGACACAGAATT
 AGGGAAATTCTCACCTGATAGGAGATAAAGTCCTGAACCTACCTGTTCAAAACTCCTCTGTCTTAA
 211 D S L K E W N Y P L F Q D L N G Q S F E E T Q N

 701 GGGTCTCTTTAACATCACCTCTCTAAAGGTCTTTTCACTCAGACATCAGAAGGAGACTTGGACGA
 CCCAGAAGAAATTGTAGTGGAGAAGAGATTATCCAGAAAAGTAGTCTGTAGTCTCCTCTGAACCTGCT
 234 D W V F F N I T S S L I G L F H Q T S E G D L D D

 771 TTTGGCTCAGGATTAAAGGACTTGTACCATACCCATCTTCTGAACCTTATCCCTGGTGAAGAT
 AAACCGAGTCCTAACATTCTGAACATGGTATGGGTAGAAAAGACTTGAAAATAGGGAAACCACCTCTA
 257 D L A Q D L K D L Y H T P S F L N F Y P L G E D

Fig.2A

841 ATTGACATTATTTTAACCTGAAAAGCACCTTCACAGAACCTGTCTGGAGGAAGGACCAACACCATC
TAACGTAAATAAAATTGAACCTTTCGAGTGTCTGGACAGGACACCTCCTGGTTGGTAG
281> ! D ! ! F N L K S T F T E P V L W R K D Q H H

911 ACCCGCGTGGAGCAGCTGACCCCTGAATGGCCTCCTGCAGGCTCTCAGAGCCCCCTGCATCATGAGGGGA
TGGCGCACCTCGACTGGACCTACCGGAGGACGTCCGAGAAGTCTGGGACGTAGTAACCTGGGCT
304> H R V E Q L T L N G L L Q A L Q S P C I I E (G E)

981 ATCTGGCAAAGGCAAGTCCACTCTGCTGCAGCGAATGCCATGCTCTGGGCTCCGAAAGTGAAGGCT
TAGACCGTTCCGTTCAAGGTGAGACGAGTCGCTTAACGGTACGAGACCCCAGGCCCTCACGGTCCGA
327> S G K G K S T L L) Q R I A M L W G S G K C K A

1051 CTGACCAAGTTCAAATTGTCTCTCCGTCTCAGCAGGGCCAGGGTGGACTTTTGAAACCCCTCT
GACTGGTCAAGTTAACGAGAAGGAGGCAGAGTCGTCGGGCTCCACCTGAAAAACTTGGGAGA
351> L T K F K F V F F L R L S R A Q G G L F E T L

1121 GTGATCAACTCCTGGATATACCTGGACAATCAGGAAGCAGACATTGATGGCCATGCTGCTGAAGCTGCG
CACTAGTTGAGGACCTATATGGACCGTGTAGTCCTCGTCTGTAAGTACCGTACGACGACTTCGACGC
374> C D Q L L D ! P G T ! R K Q T F M (A M L L K L R)

1191 CCAGAGGGTCTTCTCTGATGGCTACAATGAATTCAAGCCCCAGAAACTGCCAGAAATCGAACCC
CGTCTCCAAGAAAAGGAAGAACTACCGATGTTACTTAAGTCGGGTCTTGACGGGTCTTAGCTTCGG
397> Q R V L F L L D G Y N E) F K P Q N C P E I E A

1261 CTGATAAAGGAAAACCACCGCTCAAGAACATGGTCATCGTACCACTACCACTGAGTGCTGAGGCACA
GACTATTCTTGTGGCGAAGTCTTGTACCACTAGCAGTGGTATGGTACTCACGGACTCCGTGT
421> L I K E N H R F K N M V I V T T T T E C L R H

1331 TACGGCAGTTGGTCCCTGACTGCTGAGGTGGGGATATGACAGAACAGCGCCAGGCTCTCATCCG
ATGCCGTCAAACCACGGGACTGACGACTCCACCCCTATACTGTCCTGCGGGTCCGAGAGTAGGC
444> I R Q F G A L T A E V G D M T E D S A Q A L I R

1401 AGAAGTGCTGATCAAGGAGCTGCTGAAGGCTTGTGCTCAAATTCAAGAACCCAGGTGCTGAGGAAT
TCTTCACGACTAGTCCTCGAACGACTCCGAACACGAGGTAAAGTCTTAGGTCCACGAACCTTA
467> E V L I K E L A E G L L L Q I Q K S R C L R N

1471 CTCATGAAGACCCCTCTTGTGGTCATCACTTGTCAATCCAGATGGGTGAAAGTGAGTCCACTCTC
GAGTACTTCTGGGAGAGAAACACCACTAGTGAACACGTTAGGTCTACCCACTTCACTCAAGGTGAGAG
491> L M K T P L F V V I T C A I Q M G E S E F H S

1541 ACACACAAACACGCTTCCATACCTCTATGATCTGTTGATACAGAAAAACAAACACAAACATAAGG
TGTGTGTTGTTGCGACAAGGTATGGAAGATACTAGACAACTATGTCTTTGTTGTATTCC
514> H T Q T T L F H T F Y D L L I Q K N K H K H K G

1611 TGTGGCTGCAAGTGAATTCACTCGGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGGTGTCTCC
ACACCGACGTTCACTGAAGTAAGCCTCGGACCTGGTACACCTCTGGATCGAGACCTCCACACAAGAGG
537> V A A S D F ! R S L D H C G D L A L E G V F S

1681 CACAAGTTGATTCGAACCTGAGGATGTGCTCAGCGTGAATGAGGATGTCTGCTGACAACACTGGGCTCC
GTGTTCAAACCTAAAGCTTGACGTCCTACACAGGTGCGACTTACTCCTACAGGACGACTGTTGACCCGAGG
561> H K F D F E L Q D V S S V N E D V L L T T G L

Fig.dB

1751 TCTGTAAATACAGCTCAAAGGTTCAAGCCAAAGTATAAATTCTTCACAAGTCATTCCAGGAGTACAC
 AGACATTATATGTCGAGTTCCAAGTCGGTTCATATTAAAGAAAGTGTCAAGGCCTCATGTG
 584^D L C K Y T A Q R F K P K Y K F F H K S F Q E Y T
 1821 AGCAGGACGAAGACTCAGCAGTTATTGACGTCTCATGAGGCCAGAGGAGGTGACCAAGGGAAATGGTTAC
 TCGTCCTGCTCTGAGTCGTCAAATAACTGCAGAGTACTCGGTCTCTCCACTGGTCCCTACCAATG
 607^D A G R R L S S L L T S H E P E E V T K G N G Y
 1891 TTGCAGAAAATGGTTCCATTGAGCATTACATCCACTTATAGCAGCCTGCTCCGGTACACCTGTGGGT
 AACGTCTTTACCAAAGGTAAGCCTGTAATGTAGGTGAATATCGTCGGACGAGGCATGTGGACACCCA
 631^D L Q K M V S ! S D ! T S T Y S S L L R Y T C G
 1961 CATCTGTGGAAGCCACCAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCCCTCGG
 GTAGACACCTTCGGGGTCCCACAATACTCGTGGAGCGTCGTACATAGTTGTGCCGACGGAAGAGCC
 654^D S S V E A T R A V M K H L A A V Y Q H G C L L G
 2031 ACTTCCATGCCAACAGGGCTCTCTGGAGACAGGAATCTTGCAAAGTGTGAAAAACACCACTGAGCAA
 TGAAAGGTAGCGGTCTCCGGAGAGACCTCTGCTTAGAAACGTTACACTTTGTGGTACTCGTT
 677^D L S I A K R P L W R Q E S L Q S V K N T T E Q
 D
 2101 GAAATTCTGAAAGCCATAAACATCAATTCTTGTAGAGTGTGGCATCCATTATCAAGAGAGTACAT
 CTITAAGACTTCGGTATTGTAGTTAAGGAAACATCTCACACCGTAGGTAATATAGTTCTCATGTA
 701^D E I L K A I N I N S F V E C G I H L Y Q E S T
 N
 2171 CCAAATAGCCCTGAGCCAAGAATTGAAGCTTCTCAAGGTAAAAGCTTATATCAACTCAGGGAA
 GGTAGTCGGACTCGGTTCTAAACTCGAAAGAAAGTCCATTTCGAATATATAGTTGAGTCCCTT
 724^D S K S A L S Q E F E A F F Q G K S L Y I N S G N
 H
 2241 CATCCCCGATTACTTATTGACTTCTTGAACATTGCCAATTGTCAAGTGTGCCCTGGACTTCATTAAA
 GTAGGGGCTAATGAATAACTGAAGAAACTGTAAACGGGTTAACACGTTACGGGACCTGAAGTAATT
 747^D I P D Y L F D F F E H L P N C A S A L D F I K
 O
 2311 CTGGACTTTATGGGGGAGCTATGGCTCATGGAAAAGGCTGCAGAAGACACAGGTGGAATCCACATGG
 GACCTGAAAATACCCCTCGATACCGAAGTACCCCTTCCGACGTCTCTGTGTCCACCTTAGGTGTACC
 771^D L D F Y G G A M A S W E K A A E D T G G I H M
 2381 AAGAGGCCAACCTACATTCCCAGCAGGGCTGATCTTGTCTCACTGGAAGCAGGAATTCAAG
 TTCTCCGGGTCTTGGATGTAAGGGCTCCGACATAGAACAGTGTGACCTCGCCTTAAGTC
 794^D E E A P E T Y I P S R A V S L F F N W K Q E F R
 2451 GACTCTGGAGGTCACACTCCGGGATTCAGCAAGTGAATAAGCAAGATATCAGATATCTGGGGAAAATA
 CTGAGACCTCCAGTGTGAGGCCCTAAAGTCGTTCAACTTATTGTTCTATAGTCTATAGACCCCTTTAT
 817^D T L E V T L R D F S K L N K Q D I R Y L G K I
 2521 TTCAGCTCTGCCACAAGCCTCAGGCTGCAAATAAGAGATGTGCTGGTGTGGCTGGAAGCCTCAGTTGG
 AAGTCGAGACGGTGGACATCTGTAAATAAGAGAGTACCACTTCGGTCAGGGAGTGGTATCTCTACTCTC
 841^D F S S A T S L R L Q I K R C A G V A G S L S L
 2591 TCCTCAGCACCTGTAAGAACATTATTCTCATGGTGAAGCCAGTCCCTCACCATAGAACAGTGGAGAG
 AGGAGTCGAGACGGTGGACATCTGTAAATAAGAGAGTACCACTTCGGTCAGGGAGTGGTATCTCTACTCTC
 864^D V L S T C K N I Y S L M V E A S P L T I E D E R

Fig.dC

2661 GCACATCACATCTGTAACAAACCTGAAAACCTTGGAGTATTGACCTACAGAACATCAACGGCTGCCGGT
 CGTAGCTGAGACATTGTTGGACTTTGGAACTCATAAGTACTGGATGTCAGTTGCCAACGGCCA
 887D H I T S V T N L K T L S I H D L Q N Q R L P G

2731 GGTCTGACTGACAGCTTGGTAACCTGAAGAACCTTACAAGCTCATAATGGATAACATAAAGATGAATG
 CCAGACTGACTGTCGAACCCATTGAACCTCTTGGATGTTGGAGTATTACCTATTGTATTCTACTTAC
 911D G L T D S L G N L K N L T K L I M D N I K M N

2801 AAGAAGATGCTATAAAACTAGCTGAAGGCCTGAAAAACCTGAAGAAGATGTGTTATTCATTTGACCCA
 TTCTCTACGATATTGATCGACTTCCGACTTTGGACTCTTCTACACAAATAAGTAAACTGGGT
 934D E E D A I K L A E G L K N L K K M C L F H L T H

2871 CTTGTCTGACATTGGAGAGGGATGGATTACATAGTCAGTCAGTGAAACCTGTGACCTTGAA
 GAACAGACTGTAACCTCTCCCTACCTAATGTATCAGTCAGAGACAGTCAGTGGACACTGGAACTT
 957D L S D I G E G M D Y I V K S L S S E P C D L E

2941 GAAATTCAATTAGTCCTGCTGCTTGTCTGCAAATGCAAGTGGAAAATCCTAGCTCAGAACATCTTCACAATT
 CTTCAGGTTAACATCAGAGGACGACGAAACAGACGTTACGTCACTTTAGGATCGAGTCAGTTAGTAA
 981D E I Q L V S C C L S A N A V K I L A Q N L H N

3011 TGGTCAAACGTGAGCATTCTGATTTATCAGAAAATTACCTGGAAAAGATGGAAATGAAGCTCTCATGA
 ACCAGTTGACTCGTAAGAACTAAATAGTCAGTTAGGATCGAGTCAGTTAGTAA
 3004D L V K L S I L D L S E N Y L E K D G N E A L H E

3081 ACTGATCGACAGGATGAACGTCTAGAACAGCTACCGCACTGATGCTGCCCTGGGCTGTGACGTGCAA
 TGACTAGCTGCTACTTGACGATCTGCGAGTGGCGTACTACGACGGGACCCGACACTGCACGTT
 3027D L I D R M N V L E Q L T A L M L P W G C D V Q

3151 GGCAGCTGAGCAGCTGTTGAAACATTGGAGGAGGTCCCACAACCTCGTCAAGCTGGGTGAAAAGT
 CGTCGGACTCGTGGACAACCTTGTAAACCTCCAGGGTGTGAGCAGTCAGCTAACCTTGA
 1051D G S L S S L L K H L E E V P Q L V K L G L K N

3221 GGAGACTCACAGATAACAGAGATTAGAATTAGGTGCATTTTGAAAGAACCTCTGAAAAGT
 CCTCTGAGTGTCTATGTCTAACTTAAACCGCTTACGACACTCGTCACTACCTACCGAACGGAGTACCCACATAACTCTA
 1074D W R L T D T E I R I L G A F F G K N P L K N F Q

3291 GCAGTTGAATTGGCGGGAAATCGTGTGAGCAGTGTGGATGGCTTGCCTTCATGGGTGATTGAGAAT
 CGTCAACTAAACCGCCCTTACGACACTCGTCACTACCTACCGAACGGAGTACCCACATAACTCTA
 1097D Q L N L A G N R V S S D G W L A F M G V F E N

3361 CTTAAGCAATTAGTGTGTTGACTTGTACTAAAGAATTCTACCTGATCCAGCATTAGTCAGAAAAC
 GAATTGTTAACAAAAACTGAAATCATGATTCTAAAGATGGACTAGGTGTAATCAGTCAGTTG
 1121D L K Q L V F F D F S T K E F L P D P A L V R K

3431 TTAGCCAAGTGTATTCCAAGTTAACCTTCTGCAAGAACAGCTAGGCTGTTGGGTGCGAATTGATGATGA
 AATCGGTTCACAATAGGTCAATTGAAAAGACGTTCTCGATCCGAAACACCCACCGTAAACTACTACT
 1144D L S Q V L S K L T F L Q E A R L V G W Q F D D D

3501 TGATCTCAGTGTATTACAGATGAGAACAGCTCAGATGATTGCCATGGGTATAAAACTACTTCCTTAC
 ACTAGAGTCACAATAATGTCTACTCTTGTGAGTCACTAAACGGGTACCCAAATATTGATGAGGAATG
 1167D D L S V I T D E K A Q M I C P W V I K L L P Y

Fig. d D

3571 ACAGTGGCAGCATCAGAACTGGAATTAGATCTCTGCCTCTAG
TGTACCCGTCGTAGTCTTGACCTTAAGTCTAGAGAACGGAGGATC
1191► T V A A S E L E F R S L A S -----

00 00 00 00 00 00 00 00 00 00 00 00 00 00 00 00

Fig. 2E

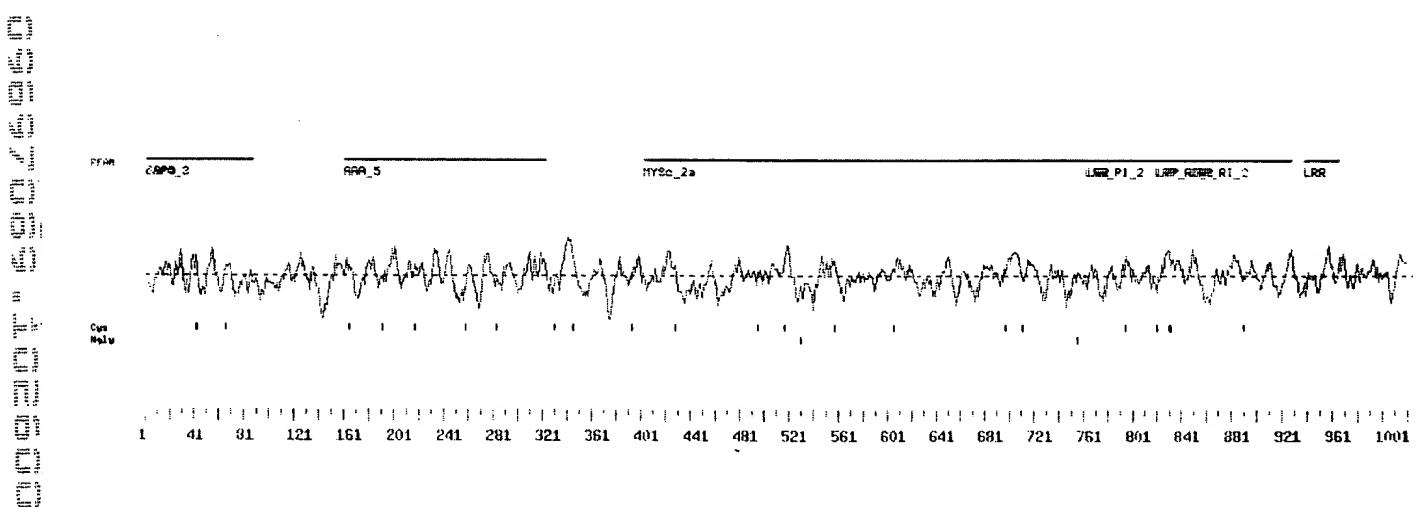


Fig. 3

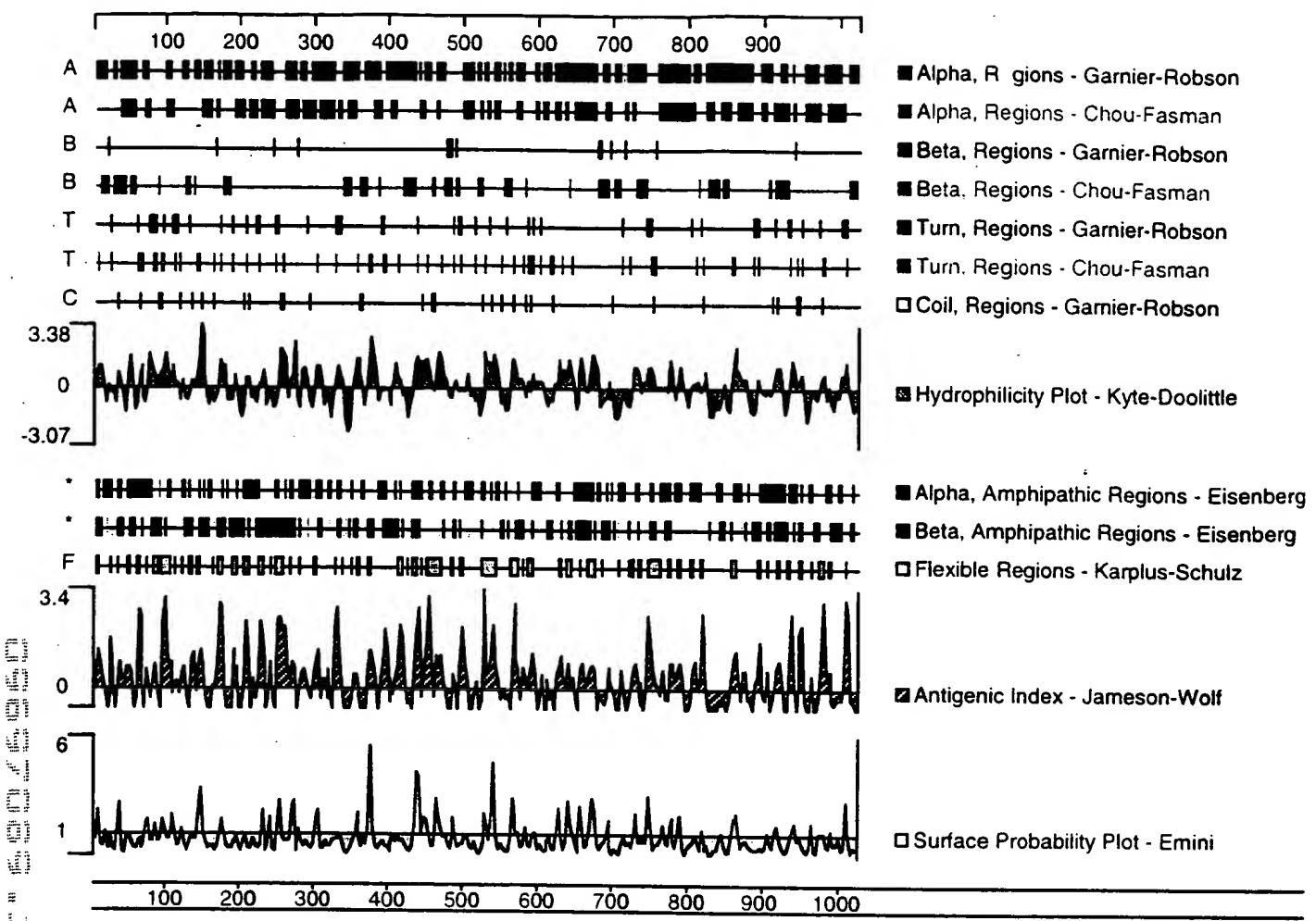


Fig. 4

CARD: domain 1 of 1, from 2 to 88: score 16.0, E = 0.0065
 SEQ ID NO: 7 *->aeddrrl1rknrllellgeltlsg1LdhLleknvLteeeeEkikaknt
 CARD12 2 --NFIKDNSRALIQRMGMTVIKQITDDLFWVNVLNREEVNIICCEKV 46

trrdkareLiDsvqkkGnqAfqiFlqaLretdqellad111de--*
 ++ d ar i +++kkG++ +++F1 +L+e ++ l +dl +
 CARD12 47 EQ-DAARGIIHMLKKGSESCNLFLKSLKEWNYPLFQDLNGQS 88

Fig. 5A

LRR: domain 1 of 4, from 764 to 791: score 0.6, E = 8.2e+02
 SEQ ID NO: 8 *->nLeeLdLsnN.Lt.....slppglfsnLp--*
 nL++L ++n + +++ +1 +g ++nL+
 CARD12 764 NLTKLIMDNIKMNeedaiKLAEG-LKUNK 791

Fig. 5B

LRR: domain 2 of 4, from 821 to 848: score 0.3, E = 9.3e+02
 SEQ ID NO: 8 *->nLeeLdLsnN.Lt.....slppglfsnLp--*
 Lee+ L ++ L+ + ++ +nL
 CARD12 821 DLEEIQLVSCcLSanavKILAQNLLHNLV 848

Fig. 5C

LRR: domain 3 of 4, from 849 to 872: score 11.2, E = 23
 SEQ ID NO: 8 *->nLeeLdLsnN.LtslppglfsnLp--*
 +L LdLs N L++ +++++ L
 CARD12 849 KLSILDLSENyLEKDGNEALHELI 872

Fig. 5D

LRR: domain 4 of 4, from 938 to 965: score 4.2, E = 2.5e+02
 SEQ ID NO: 8 *->nLeeLdLsnN.Lt.....slppglfsnLp--*
 n + L+L +N+ +++++ + +f+nL+
 CARD12 938 NFQQNLNLAGNrVSsdgw1AFMG-VFENLK 965

Fig. 5E

E . L . L L . S . . . E G E . G . G K . . L L . . I A . L W . S G Consensus #1
E Q L V L N G V L G A L N S V C I V E G E A G S G K S V L L Q K I A F L W G S G Majority

10 20 30 40

1 E Q L T L N G L L Q A L Q S P C I I E G E S G K G K S T L L Q R I A M L W G S G CARD12-C
1 E P L V L P E V F G N L N S V M C V E G E A G S G K T V L L K K I A F L W A S G NAIP-C (SEQIDNO:9)

. C . . L . . F . . V F . L . L S . . R . . . G L . . . C D Q L L . . . G . . Consensus #1
K C K A L T K F K F V F F L R L S - - R A Q G G L F E T L C D Q L L D I P G T I Majority

50 60 70 80

41 K C K A L T K F K F V F F L R L S - - R A Q G G L F E T L C D Q L L D I P G T I CARD12-C
41 C C P L L I N R F Q L V F Y L S L S S T R P D E G L A S I I C D O L L E K E G S V NAIP-C

. L . . . V L F L L D . Y . E C I . . L Consensus #1
T E Q T F R A I L L Q L K N Q V L F L L D G Y N E I K P Q N C S I P Q V I G A L Majority

90 100 110 120

79 R K Q T F M A M L L K L R Q R V L F L L D G Y N E F K P Q N C P E - - - I E A L CARD12-C
81 T E M C M R N I I Q Q L K N Q V L F L L D D Y K E I - - - C S I P Q V I G K L NAIP-C

I . . N H T . . . R . I R E Consensus #1
I Q E N H L S K T C V L V A V T T E R A R D I R Q F G A L I A E V G A F T E D S Majority

130 140 150 160

116 I K E N H R F K N M V I V T T T E C L R H I R Q F G A L T A E V G D M T E D S CARD12-C
117 I Q K N H L S R T C L L I A V R T N R A R D I R R Y L E T I L E I Q A F P F Y N NAIP-C

. . . . R K L K T P L F V . Consensus #1
A V A L L R E V L I K E L A E L R G L L V Q I G K S Q S L Q N L Q K T P L F V A Majority

170 180 190 200

156 A Q A L I R E V L I K E L A E - - G L L L Q I Q K S R C L R N L M K T P L F V V CARD12-C
157 T V C I L R K L F S H N M T R L R K F M V Y F G K N Q S L Q K I Q K T P L F V A NAIP-C

C . . C A F F L . . . N K Consensus #1
C A I C A I Q W G E S E F D S S F T D V A V F K S F Y D L L I L K N K H K H K G V Majority

210 220 230 240

194 I T C A I Q M G E S E F H S H - T Q T T L F H T F Y D L L I Q K N K H K H K G V CARD12-C
197 A I C A - H W F Q Y P F D P S F D D V A V F K S Y M E R L S L R N K - - - - - NAIP-C

A C G . L A L . G . F S . . F . F . . D V . E Consensus #1
A A A D I L K A T V S S C G D L A L E G V F S H K F D F E L D D V A E A G V D E Majority

250 260 270 280

233 A A S D F I R S - L D H C G D L A L E G V F S H K F D F E L Q D V S - - S V N E CARD12-C
230 A T A E I L K A T V S S C G E L A L K G F F S C C F E E N D D D L A E A G V D E NAIP-C

D . . L T . . L . . K . T A Q R . . P . Y . F . . . F Q E . . A G . R L . . L Consensus #1
D V L L T T G L L C K Y T A Q R F K P K Y K F F H K S F Q E Y T A G R R L S S L Majority

290 300 310 320

270 D V L L T T G L L C K Y T A Q R F K P K Y K F F H K S F Q E Y T A G R R L S S L CARD12-C
270 D E D L T M C L M S K F T A O R L R P F Y R F L S P A F O E F L A G M R L I E L NAIP-C

Fig.6A

Fig. 6B

Consensus 'Consensus #1': When all match the residue of CARD12-C show the residue of CARD12-C, otherwise show '...'.

Decoration 'Decoration #1': Box residues that match the consensus named 'Consensus #1' exactly.

Fig. 6C